

Rec'd PCT/PTO 02 AUG 2005
10/511989

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/511,989A
Source: PG 110
Date Processed by STIC: 8/2/05

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PCT

RAW SEQUENCE LISTING

DATE: 08/02/2005

PATENT APPLICATION: US/10/511,989A

TIME: 15:07:06

Input Set : A:\5470.368.ST25.txt

Output Set: N:\CRF4\08022005\J511989A.raw

3 <110> APPLICANT: Ting, Jenny
 4 Linhoff, Michael
 5 Harton, Johnathan
 6 Williams, Kristi
 7 Lich, John
 8 O'Connor, William
 9 Moore, Christopher
 10 Davis, Beckley
 11 Brickey, W. Jane
 12 Conti, Brian
 13 Zhang, Jinghua
 14 Zhu, Xin-Sheng
 16 <120> TITLE OF INVENTION: CATERPILLER GENE FAMILY
 18 <130> FILE REFERENCE: 5470-368
 20 <140> CURRENT APPLICATION NUMBER: US 10/511,989A
 C--> 21 <141> **CURRENT FILING DATE: 2004-10-21**
 23 <150> PRIOR APPLICATION NUMBER: PCT/US03/13562
 24 <151> PRIOR FILING DATE: 2003-04-30
 26 <150> PRIOR APPLICATION NUMBER: US 60/376,626
 27 <151> PRIOR FILING DATE: 2002-04-30
 29 <160> NUMBER OF SEQ ID NOS: 187
 31 <170> SOFTWARE: PatentIn version 3.3
 33 <210> SEQ ID NO: 1
 34 <211> LENGTH: 3731
 35 <212> TYPE: DNA
 36 <213> ORGANISM: Homo sapiens
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 43 gtgaatgatg caatggaagg tgtgctgggg tcgccctgtg tcccgatcat aggagcatct 180
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 61 aggggaatgt gtcaacctca gccaccggtc caccggctc ctgctggtga aggagcactc 720
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166 <210> SEQ ID NO: 2
167 <211> LENGTH: 1062

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171 <400> SEQUENCE: 2
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181 Gly Thr Ala Thr Glu Leu Gly Glu Gly Lys Ile Pro Trp Gly Ser Met
182 35 40 45
185 Glu Lys Ala Gly Pro Leu Glu Met Ala Gln Leu Leu Ile Thr His Phe
186 50 55 60
189 Gly Pro Glu Glu Ala Trp Arg Leu Ala Leu Ser Thr Phe Glu Arg Ile
190 65 70 75 80
193 Asn Arg Lys Asp Leu Trp Glu Arg Gly Gln Arg Glu Asp Leu Val Arg
194 85 90 95
197 Asp Thr Pro Pro Gly Gly Pro Ser Ser Leu Gly Asn Gln Ser Thr Cys
198 100 105 110
201 Leu Leu Glu Val Ser Leu Val Thr Pro Arg Lys Asp Pro Gln Glu Thr
202 115 120 125
205 Tyr Arg Asp Tyr Val Arg Arg Lys Phe Arg Leu Met Glu Asp Arg Asn
206 130 135 140
209 Ala Arg Leu Gly Glu Cys Val Asn Leu Ser His Arg Tyr Thr Arg Leu
210 145 150 155 160
213 Leu Leu Val Lys Glu His Ser Asn Pro Met Gln Val Gln Gln Gln Leu
214 165 170 175
217 Leu Asp Thr Gly Arg Gly His Ala Arg Thr Val Gly His Gln Ala Ser
218 180 185 190
221 Pro Ile Lys Ile Glu Thr Leu Phe Glu Pro Asp Glu Glu Arg Pro Glu
222 195 200 205
225 Pro Pro Arg Thr Val Val Met Gln Gly Ala Ala Gly Ile Gly Lys Ser
226 210 215 220
229 Met Leu Ala His Lys Val Met Leu Asp Trp Ala Asp Gly Lys Leu Phe
230 225 230 235 240
233 Gln Gly Arg Phe Asp Tyr Leu Phe Tyr Ile Asn Cys Arg Glu Met Asn
234 245 250 255
237 Gln Ser Ala Thr Glu Cys Ser Met Gln Asp Leu Ile Phe Ser Cys Trp
238 260 265 270
241 Pro Glu Pro Ser Ala Pro Leu Gln Glu Leu Ile Arg Val Pro Glu Arg
242 275 280 285
245 Leu Leu Phe Ile Ile Asp Gly Phe Asp Glu Leu Lys Pro Ser Phe His
246 290 295 300
249 Asp Pro Gln Gly Pro Trp Cys Leu Cys Trp Glu Glu Lys Arg Pro Thr
250 305 310 315 320
253 Glu Leu Leu Leu Asn Ser Leu Ile Arg Lys Lys Leu Leu Pro Glu Leu
254 325 330 335
257 Ser Leu Leu Ile Thr Thr Arg Pro Thr Ala Leu Glu Lys Leu His Arg
258 340 345 350
261 Leu Leu Glu His Pro Arg His Val Glu Ile Leu Gly Phe Ser Glu Ala
262 355 360 365

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265 Glu Arg Lys Glu Tyr Phe Tyr Lys Tyr Phe His Asn Ala Glu Gln Ala
266      370      375      380
269 Gly Gln Val Phe Asn Tyr Val Arg Asp Asn Glu Pro Leu Phe Thr Met
270 385      390      395      400
273 Cys Phe Val Pro Leu Val Cys Trp Val Val Cys Thr Cys Leu Gln Gln
274      405      410      415
277 Gln Leu Glu Gly Gly Gly Leu Leu Arg Gln Thr Ser Arg Thr Thr Thr
278      420      425      430
281 Ala Val Tyr Met Leu Tyr Leu Leu Ser Leu Met Gln Pro Lys Pro Gly
282      435      440      445
285 Ala Pro Arg Leu Gln Pro Pro Asn Gln Arg Gly Leu Cys Ser Leu
286      450      455      460
289 Ala Ala Asp Gly Leu Trp Asn Gln Lys Ile Leu Phe Glu Glu Gln Asp
290 465      470      475      480
293 Leu Arg Lys His Gly Leu Asp Gly Glu Asp Val Ser Ala Phe Leu Asn
294      485      490      495
297 Met Asn Ile Phe Gln Lys Asp Ile Asn Cys Glu Arg Tyr Tyr Ser Phe
298      500      505      510
301 Ile His Leu Ser Phe Gln Glu Phe Phe Ala Ala Met Tyr Tyr Ile Leu
302      515      520      525
305 Asp Glu Gly Glu Gly Gly Ala Gly Pro Asp Gln Asp Val Thr Arg Leu
306      530      535      540
309 Leu Thr Glu Tyr Ala Phe Ser Glu Arg Ser Phe Leu Ala Leu Thr Ser
310 545      550      555      560
313 Arg Phe Leu Phe Gly Leu Leu Asn Glu Glu Thr Arg Ser His Leu Glu
314      565      570      575
317 Lys Ser Leu Cys Trp Lys Val Ser Pro His Ile Lys Met Asp Leu Leu
318      580      585      590
321 Gln Trp Ile Gln Ser Lys Ala Gln Ser Asp Gly Ser Thr Leu Gln Gln
322      595      600      605
325 Gly Ser Leu Glu Phe Phe Ser Cys Leu Tyr Glu Ile Gln Glu Glu Glu
326      610      615      620
329 Phe Ile Gln Gln Ala Leu Ser His Phe Gln Val Ile Val Val Ser Asn
330 625      630      635      640
333 Ile Ala Ser Lys Met Glu His Met Val Ser Ser Phe Cys Leu Lys Arg
334      645      650      655
337 Cys Arg Ser Ala Gln Val Leu His Leu Tyr Gly Ala Thr Tyr Ser Ala
338      660      665      670
341 Asp Gly Glu Asp Arg Ala Arg Cys Ser Ala Gly Ala His Thr Leu Leu
342      675      680      685
345 Val Gln Leu Arg Pro Glu Arg Thr Val Leu Leu Asp Ala Tyr Ser Glu
346      690      695      700
349 His Leu Ala Ala Ala Leu Cys Thr Asn Pro Asn Leu Ile Glu Leu Ser
350 705      710      715      720
353 Leu Tyr Arg Asn Ala Leu Gly Ser Arg Gly Val Lys Leu Leu Cys Gln
354      725      730      735
357 Gly Leu Arg His Pro Asn Cys Lys Leu Gln Asn Leu Arg Leu Lys Arg
358      740      745      750
361 Cys Arg Ile Ser Ser Ser Ala Cys Glu Asp Leu Ser Ala Ala Leu Ile

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362          755          760          765
365 Ala Asn Lys Asn Leu Thr Arg Met Asp Leu Ser Gly Asn Gly Val Gly
366          770          775          780
369 Phe Pro Gly Met Met Leu Leu Cys Glu Gly Leu Arg His Pro Gln Cys
370 785          790          795          800
373 Arg Leu Gln Met Ile Gln Leu Arg Lys Cys Gln Leu Glu Ser Gly Ala
374          805          810          815
377 Cys Gln Glu Met Ala Ser Val Leu Gly Thr Asn Pro His Leu Val Glu
378          820          825          830
381 Leu Asp Leu Thr Gly Asn Ala Leu Glu Asp Leu Gly Leu Arg Leu Leu
382          835          840          845
385 Cys Gln Gly Leu Arg His Pro Val Cys Arg Leu Arg Thr Leu Trp Leu
386          850          855          860
389 Lys Ile Cys Arg Leu Thr Ala Ala Cys Asp Glu Leu Ala Ser Thr
390 865          870          875          880
393 Leu Ser Val Asn Gln Ser Leu Arg Glu Leu Asp Leu Ser Leu Asn Glu
394          885          890          895
397 Leu Gly Asp Leu Gly Val Leu Leu Leu Cys Glu Gly Leu Arg His Pro
398          900          905          910
401 Thr Cys Lys Leu Gln Thr Leu Arg Leu Gly Ile Cys Arg Leu Gly Ser
402          915          920          925
405 Ala Ala Cys Glu Gly Leu Ser Val Val Leu Gln Ala Asn His Asn Leu
406          930          935          940
409 Arg Glu Leu Asp Leu Ser Phe Asn Asp Leu Gly Asp Trp Gly Leu Trp
410 945          950          955          960
413 Leu Leu Ala Glu Gly Leu Gln His Pro Ala Cys Arg Leu Gln Lys Leu
414          965          970          975
417 Trp Leu Asp Ser Cys Gly Leu Thr Ala Lys Ala Cys Glu Asn Leu Tyr
418          980          985          990
421 Phe Thr Leu Gly Ile Asn Gln Thr Leu Thr Asp Leu Tyr Leu Thr Asn
422          995          1000          1005
425 Asn Ala Leu Gly Asp Thr Gly Val Arg Leu Leu Cys Lys Arg Leu
426          1010          1015          1020
429 Ser His Pro Gly Cys Lys Leu Arg Val Leu Trp Leu Phe Gly Met
430          1025          1030          1035
433 Asp Leu Asn Lys Met Thr His Ser Arg Leu Ala Ala Leu Arg Val
434          1040          1045          1050
437 Thr Lys Pro Tyr Leu Asp Ile Gly Cys
438          1055          1060
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444 <213> ORGANISM: Homo sapiens
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451 gtgaatgatg caatggaagg tgtgctgggg tcgacctgtg tcccgatgat aggagcatct 180
453 cagcctccag gtcctctcct ttggggctta cggcaccgcc atgctacgaa ccgcaggcag 240
455 ggacggcctc tgctgcctgt ccacctactt ggaagaactc gaggctgtgg aactgaagaa 300

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 08/02/2005
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:92; Xaa Pos. 2,3,4,5,8
Seq#:93; Xaa Pos. 2,3
Seq#:94; Xaa Pos. 1,2,3,4
Seq#:95; Xaa Pos. 1,3
Seq#:150; Xaa Pos. 1,6,8,11,18,19,20,21,23,26,28,30
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Seq#:152; Xaa Pos. 1,3,4,5,7,13
Seq#:153; Xaa Pos. 3,7,9,20,23,25
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Seq#:154; Xaa Pos. 30,31
Seq#:155; Xaa Pos. 2,3,5,6,7,8,9,10,12,13,15,16,17,19,22,23,26,29,30,32,33
Seq#:155; Xaa Pos. 35,36,37
Seq#:156; Xaa Pos. 2,4,5,6,7,8,9,10,11,12,13,14
Seq#:157; Xaa Pos. 2,3,6,12,14,15,16,17,18,20,21,22,25,26,27,30,31,32,33,34
Seq#:157; Xaa Pos. 35,36,39,40,41,42,43
Seq#:158; Xaa Pos. 2,4,7,8,12,15,16,18
Seq#:159; Xaa Pos. 7,8,10,11,12,15,16,19,20,21,23,24,25,26
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Seq#:165; Xaa Pos. 74,136,232
Seq#:176; Xaa Pos. 178,347

VERIFICATION SUMMARY

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L:6739 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:93 after pos.:0
L:6759 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:94 after pos.:0
L:6784 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:95 after pos.:0
L:7831 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:150 after pos.:0
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L:7920 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:151 after pos.:0
M:341 Repeated in SeqNo=151
L:7964 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:152 after pos.:0
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L:10514 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:176 after pos.:176
M:341 Repeated in SeqNo=176